



~4881809.txt
SEQUENCE LISTING

<110> DIDEBERG, OTTO
VERNET, THIERRY
MOUZ, NICOLAS

<120> STREPTOCOCCUS PNEUMONIAE PBP2X MINI-PROTEIN AND USES
THEREOF

<130> 70457-19

<140> 10/520,655

<141> 2005-03-07

<150> PCT/IB03/003397

<151> 2003-07-11

<150> FR 02/08724

<151> 2002-07-11

<160> 18

<170> PatentIn Ver. 3.3

<210> 1

<211> 551

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
mini-PBP2x construct

<400> 1

Gly Ser Gly Ala Lys Arg Gly Thr Ile Tyr Asp Arg Asn Gly Val Pro
1 5 10 15

Ile Ala Glu Asp Ala Thr Ser Gly Gly Pro Asn Arg Ser Tyr Pro Asn
20 25 30

Gly Gln Phe Ala Ser Ser Phe Ile Gly Gly Gly Met Glu Ser Ser Leu
35 40 45

Asn Ser Ile Leu Ala Gly Gly Gly Gly Asp Gly Lys Asp Val Tyr Thr
50 55 60

Thr Ile Ser Ser Pro Leu Gln Ser Phe Met Glu Thr Gln Met Asp Ala
65 70 75 80

Phe Gln Glu Lys Val Lys Gly Lys Tyr Met Thr Ala Thr Leu Val Ser
85 90 95

Ala Lys Thr Gly Glu Ile Leu Ala Thr Thr Gln Arg Pro Thr Phe Asp
100 105 110

Ala Asp Thr Lys Glu Gly Ile Thr Glu Asp Phe Val Trp Arg Asp Ile
115 120 125

Leu Tyr Gln Ser Asn Tyr Glu Pro Gly Ser Thr Met Lys Val Met Met
130 135 140

Leu Ala Ala Ala Ile Asp Asn Asn Thr Phe Pro Gly Gly Glu Val Phe
145 150 155 160

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Asn Ser Ser Glu Leu Lys Ile Ala Asp Ala Thr Ile Arg Asp Trp Asp
165 170 175
Val Asn Glu Gly Leu Thr Gly Gly Arg Met Met Thr Phe Ser Gln Gly
180 185 190
Phe Ala His Ser Ser Asn Val Gly Met Thr Leu Leu Glu Gln Lys Met
195 200 205
Gly Asp Ala Thr Trp Leu Asp Tyr Leu Asn Arg Phe Lys Phe Gly Val
210 215 220
Pro Thr Arg Phe Gly Leu Thr Asp Glu Tyr Ala Gly Gln Leu Pro Ala
225 230 235 240
Asp Asn Ile Val Asn Ile Ala Gln Ser Ser Phe Gly Gln Gly Ile Ser
245 250 255
Val Thr Gln Thr Gln Met Ile Arg Ala Phe Thr Ala Ile Ala Asn Asp
260 265 270
Gly Val Met Leu Glu Pro Lys Phe Ile Ser Ala Ile Tyr Asp Pro Asn
275 280 285
Asp Gln Thr Ala Arg Lys Ser Gln Lys Glu Ile Val Gly Asn Pro Val
290 295 300
Ser Lys Asp Ala Ala Ser Leu Thr Arg Thr Asn Met Val Leu Val Gly
305 310 315 320
Thr Asp Pro Val Tyr Gly Thr Met Tyr Asn His Ser Thr Gly Lys Pro
325 330 335
Thr Val Thr Val Pro Gly Gln Asn Val Ala Leu Lys Ser Gly Thr Ala
340 345 350
Gln Ile Ala Asp Glu Lys Asn Gly Gly Tyr Leu Val Gly Leu Thr Asp
355 360 365
Tyr Ile Phe Ser Ala Val Ser Met Ser Pro Ala Glu Asn Pro Asp Phe
370 375 380
Ile Leu Tyr Val Thr Val Gln Gln Pro Glu His Tyr Ser Gly Ile Gln
385 390 395 400
Leu Gly Glu Phe Ala Asn Pro Ile Leu Glu Arg Ala Ser Ala Met Lys
405 410 415
Asp Ser Leu Asn Leu Gln Thr Thr Ala Lys Ala Leu Glu Gln Val Ser
420 425 430
Gln Gln Ser Pro Tyr Pro Met Pro Ser Val Lys Asp Ile Ser Pro Gly
435 440 445
Asp Leu Ala Glu Glu Leu Arg Arg Asn Leu Val Gln Pro Ile Val Val
450 455 460
Gly Thr Gly Thr Lys Ile Lys Asn Ser Ser Ala Glu Glu Gly Lys Asn
465 470 475 480
Leu Ala Pro Asn Gln Gln Val Leu Ile Leu Ser Asp Lys Ala Glu Glu
485 490 495

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Val Pro Asp Met Tyr Gly Trp Thr Lys Glu Thr Ala Glu Thr Leu Ala
500 505 510

Lys Trp Leu Asn Ile Glu Leu Glu Phe Gln Gly Ser Gly Ser Thr Val
515 520 525

Gln Lys Gln Asp Val Arg Ala Asn Thr Ala Ile Lys Asp Ile Lys Lys
530 535 540

Ile Thr Leu Thr Leu Gly Asp
545 550

<210> 2

<211> 46

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
primer

<400> 2

gtcgacttag tctcctaaag ttaatttaat ttttttaatg tttttg

46

<210> 3

<211> 21

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthetic
primer

<400> 3

ggatccggga caggcactcg c

21

<210> 4

<211> 43

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
primer

<400> 4

cataaatagt cccacgtttg gccccggatc cacgcggaac cag

43

<210> 5

<211> 51

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthetic
primer

<400> 5

gtttgggtaa ctacgattgg gacctccaga ggttgcattc tcagcaatcg g 51

<210> 6
<211> 48
<212> DNA
<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthetic
primer

<400> 6
gttcaaggaa ctctccattc caccgccgat aaaactagaa gcaaattg 48

<210> 7
<211> 49
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
primer

<400> 7
tgtataaaca tccttaccgt cccacctcc ccctgcaaga atactgttc 49

<210> 8
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
primer

<400> 8
ccgcatatgg ccaaacgtgg gactatttat 30

<210> 9
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
primer

<400> 9
ggctcgagtt agtctcctaa agttaatgta at 32

<210> 10
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<220>
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<222> (3)
<223> variable amino acid

<220>
<221> MOD_RES
<222> (4)
<223> hydrophobic amino acid

<220>
<221> MOD_RES
<222> (5)
<223> variable amino acid

<220>
<221> MOD_RES
<222> (6)
<223> Asp or Ser

<220>
<221> MOD_RES
<222> (10)..(12)
<223> variable amino acid

<400> 10
Arg Gly Xaa Xaa Xaa Xaa Arg Ser Gly Xaa Xaa Xaa Ala
1 5 10

<210> 11
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<220>
<221> MOD_RES
<222> (1)
<223> Arg or Lys

<220>
<221> MOD_RES
<222> (2)..(3)
<223> variable amino acid

<220>
<221> MOD_RES
<222> (5)
<223> variable amino acid

<400> 11
Xaa Xaa Xaa Pro Xaa Gly
1 5

<210> 12
<211> 10
<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<220>

<221> MOD_RES

<222> (1)

<223> Gly or Tyr

<220>

<221> MOD_RES

<222> (2)

<223> hydrophobic amino acid

<220>

<221> MOD_RES

<222> (4)..(6)

<223> variable amino acid

<220>

<221> MOD_RES

<222> (8)..(9)

<223> variable amino acid

<400> 12

Xaa Xaa Glu Xaa Xaa Xaa Asp Xaa Xaa Leu
1 5 10

<210> 13

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<220>

<221> MOD_RES

<222> (1)

<223> hydrophobic amino acid

<220>

<221> MOD_RES

<222> (2)..(3)

<223> variable amino acid

<220>

<221> MOD_RES

<222> (4)

<223> Ser or Thr

<220>

<221> MOD_RES

<222> (5)

<223> hydrophobic amino acid

<220>

<221> MOD_RES

<222> (7)..(9)

<223> variable amino acid

<400> 13

Xaa Xaa Xaa Xaa Xaa Asp Xaa Xaa Xaa Gln
1 5 10

<210> 14

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<220>

<221> MOD_RES

<222> (2)

<223> Gly or Ser

<220>

<221> MOD_RES

<222> (4)..(5)

<223> hydrophobic amino acid

<220>

<221> MOD_RES

<222> (6)..(9)

<223> variable amino acid

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<222> (12)

<223> variable amino acid

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<221> MOD_RES

<222> (13)

<223> hydrophobic amino acid

<220>

<221> MOD_RES

<222> (14)

<223> Asp or Asn

<400> 14

Thr Xaa Glu Xaa Xaa Xaa Xaa Xaa Ser Pro Xaa Xaa Xaa
1 5 10

<210> 15

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<220>

<221> MOD_RES

<222> (1)

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<222> (4)

<223> Ala or Gly

<220>

<221> MOD_RES

<222> (6)..(7)

<223> variable amino acid

<400> 15

Xaa Glu Pro Xaa Ser Xaa Xaa Lys
1 5

<210> 16

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<220>

<221> MOD_RES

<222> (1)

<223> hydrophobic amino acid

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<222> (2)..(3)

<223> variable amino acid

<220>

<221> MOD_RES

<222> (5)

<223> variable amino acid

<220>

<221> MOD_RES

<222> (7)

<223> hydrophobic amino acid

<400> 16

Xaa Xaa Xaa Ser Xaa Asn Xaa
1 5

<210> 17

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 17

Ala Lys Arg Gly Thr Ile Tyr
1 5

<210> 18
 <211> 750
 <212> PRT
 <213> Streptococcus pneumoniae

<400> 18
 Met Lys Trp Thr Lys Arg Val Ile Arg Tyr Ala Thr Lys Asn Arg Lys
 1 5 10 15
 Ser Pro Ala Glu Asn Arg Arg Arg Val Gly Lys Ser Leu Ser Leu Leu
 20 25 30
 Ser Val Phe Val Phe Ala Ile Phe Leu Val Asn Phe Ala Val Ile Ile
 35 40 45
 Gly Thr Gly Thr Arg Phe Gly Thr Asp Leu Ala Lys Glu Ala Lys Lys
 50 55 60
 Val His Gln Thr Thr Arg Thr Val Pro Ala Lys Arg Gly Thr Ile Tyr
 65 70 75 80
 Asp Arg Asn Gly Val Pro Ile Ala Glu Asp Ala Thr Ser Tyr Asn Val
 85 90 95
 Tyr Ala Val Ile Asp Glu Asn Tyr Lys Ser Ala Thr Gly Lys Ile Leu
 100 105 110
 Tyr Val Glu Lys Thr Gln Phe Asn Lys Val Ala Glu Val Phe His Lys
 115 120 125
 Tyr Leu Asp Met Glu Glu Ser Tyr Val Arg Glu Gln Leu Ser Gln Pro
 130 135 140
 Asn Leu Lys Gln Val Ser Phe Gly Ala Lys Gly Asn Gly Ile Thr Tyr
 145 150 155 160
 Ala Asn Met Met Ser Ile Lys Lys Glu Leu Glu Ala Ala Glu Val Lys
 165 170 175
 Gly Ile Asp Phe Thr Thr Ser Pro Asn Arg Ser Tyr Pro Asn Gly Gln
 180 185 190
 Phe Ala Ser Ser Phe Ile Gly Leu Ala Gln Leu His Glu Asn Glu Asp
 195 200 205
 Gly Ser Lys Ser Leu Leu Gly Thr Ser Gly Met Glu Ser Ser Leu Asn
 210 215 220
 Ser Ile Leu Ala Gly Thr Asp Gly Ile Ile Thr Tyr Glu Lys Asp Arg
 225 230 235 240
 Leu Gly Asn Ile Val Pro Gly Thr Glu Gln Val Ser Gln Arg Thr Met
 245 250 255
 Asp Gly Lys Asp Val Tyr Thr Thr Ile Ser Ser Pro Leu Gln Ser Phe
 260 265 270
 Met Glu Thr Gln Met Asp Ala Phe Gln Glu Lys Val Lys Gly Lys Tyr
 275 280 285
 Met Thr Ala Thr Leu Val Ser Ala Lys Thr Gly Glu Ile Leu Ala Thr

290 295 300

Thr Gln Arg Pro Thr Phe Asp Ala Asp Thr Lys Glu Gly Ile Thr Glu
305 310 315 320

Asp Phe Val Trp Arg Asp Ile Leu Tyr Gln Ser Asn Tyr Glu Pro Gly
325 330 335

Ser Thr Met Lys Val Met Met Leu Ala Ala Ala Ile Asp Asn Asn Thr
340 345 350

Phe Pro Gly Gly Glu Val Phe Asn Ser Ser Glu Leu Lys Ile Ala Asp
355 360 365

Ala Thr Ile Arg Asp Trp Asp Val Asn Glu Gly Leu Thr Gly Gly Arg
370 375 380

Met Met Thr Phe Ser Gln Gly Phe Ala His Ser Ser Asn Val Gly Met
385 390 395 400

Thr Leu Leu Glu Gln Lys Met Gly Asp Ala Thr Trp Leu Asp Tyr Leu
405 410 415

Asn Arg Phe Lys Phe Gly Val Pro Thr Arg Phe Gly Leu Thr Asp Glu
420 425 430

Tyr Ala Gly Gln Leu Pro Ala Asp Asn Ile Val Asn Ile Ala Gln Ser
435 440 445

Ser Phe Gly Gln Gly Ile Ser Val Thr Gln Thr Gln Met Ile Arg Ala
450 455 460

Phe Thr Ala Ile Ala Asn Asp Gly Val Met Leu Glu Pro Lys Phe Ile
465 470 475 480

Ser Ala Ile Tyr Asp Pro Asn Asp Gln Thr Ala Arg Lys Ser Gln Lys
485 490 495

Glu Ile Val Gly Asn Pro Val Ser Lys Asp Ala Ala Ser Leu Thr Arg
500 505 510

Thr Asn Met Val Leu Val Gly Thr Asp Pro Val Tyr Gly Thr Met Tyr
515 520 525

Asn His Ser Thr Gly Lys Pro Thr Val Thr Val Pro Gly Gln Asn Val
530 535 540

Ala Leu Lys Ser Gly Thr Ala Gln Ile Ala Asp Glu Lys Asn Gly Gly
545 550 555 560

Tyr Leu Val Gly Leu Thr Asp Tyr Ile Phe Ser Ala Val Ser Met Ser
565 570 575

Pro Ala Glu Asn Pro Asp Phe Ile Leu Tyr Val Thr Val Gln Gln Pro
580 585 590

Glu His Tyr Ser Gly Ile Gln Leu Gly Glu Phe Ala Asn Pro Ile Leu
595 600 605

Glu Arg Ala Ser Ala Met Lys Asp Ser Leu Asn Leu Gln Thr Thr Ala
610 615 620

Lys Ala Leu Glu Gln Val Ser Gln Gln Ser Pro Tyr Pro Met Pro Ser

625		630		635		640
Val Lys Asp Ile	Ser 645	Pro Gly Asp Leu	Ala 650	Glu Glu Leu Arg	Arg 655	Asn
Leu Val Gln	Pro 660	Ile Val Val Gly	Thr 665	Gly Thr Lys Ile	Lys 670	Asn Ser
Ser Ala Glu	Glu 675	Gly Lys Asn Leu	Ala 680	Pro Asn Gln	Gln 685	Val Leu Ile
Leu Ser Asp	Lys 690	Ala Glu Glu Val	Pro Asp Met	Tyr 700	Gly Trp Thr	Lys
Glu Thr Ala	Glu 705	Thr Leu Ala Lys	Trp Leu Asn	Ile 715	Glu Leu Glu	Phe 720
Gln Gly ser	Gly 725	Ser Thr Val Gln	Lys Gln 730	Asp Val Arg	Ala Asn 735	Thr
Ala Ile Lys	Asp 740	Ile Lys Lys Ile	Thr 745	Leu Thr Leu Gly	Asp 750	